

JUN 26 2001 1646

TECH CENTER 1600/2900

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/637,977

DATE: 06/06/2001

TIME: 14:00:08

Input Set : A:\A68110-1.app

Output Set: C:\CRF3\06062001\I637977.raw

3 <110> APPLICANT: MURRAY, RICHARD
5 <120> TITLE OF INVENTION: Novel Methods of Diagnosis of Angiogenesis,
6 Compositons, and Methods of Screening for Angiogenesis
7 Modulators
9 <130> FILE REFERENCE: A-68110-1/DJB/RMS/DCF
11 <140> CURRENT APPLICATION NUMBER: US 09/637,977
12 <141> CURRENT FILING DATE: 2000-08-11
14 <150> PRIOR APPLICATION NUMBER: US 60/148,425
15 <151> PRIOR FILING DATE: 1999-08-11
17 <160> NUMBER OF SEQ ID NOS: 22
19 <170> SOFTWARE: PatentIn Ver. 2.1
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22 <211> LENGTH: 1237
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
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29 cccgggatcg cccagcagg gatggcgac aagatctggc tgcccttccc cgtgtcctt 180
30 ctggccgctc tgctccggt gctgctgct ggggcggccg gcttcacacc ttccctcgat 240
31 agcgacttca cttttaccct tcccgcggc cagaaggagt gcttctacca gcccatgcc 300
32 ctgaaggcct cgctggagat cgagtaccaa gttttagatg gagcaggatt agatattgat 360
33 ttccatcttg cctctccaga aggcaaaacc ttagtttttg aacaaagaaa atcagatgga 420
34 gttcacactg tagagactga agttggtgat tacatgttct gctttgacaa tacattcagc 480
35 accatttctg agaagggtgat tttctttgaa ttaatcctgg ataatatggg agaacaggca 540
36 caagaacaag aagattggaa gaaatatatt actggcacag atatattgga tatgaaactg 600
37 gaagacatcc tggaatccat caacagcatc aagtccagac taagcaaaag tgggcacata 660
38 caaactctgc ttagagcatt tgaagctcgt gatcgaaaca tacaagaaag caactttgat 720
39 agagtcaatt tctggtctat ggttaattta gtggtcatgg tgggtggtgc agccattcaa 780
40 gtttatatgc tgaagagtct gtttgaagat aagaggaaaa gtagaactta aaactccaaa 840
41 ctagagtacg taacattgaa aaatgaggca taaaaatgca ataaactgtt acagtcaaga 900
42 ccattaatgg tcttctccaa aatattttga gatataaaa taggaaacag gtataatttt 960
43 aatgtgaaaa ttaagtcttc actttctgtg caagtaatcc tgctgatcca gttgtactta 1020
44 agtgtgtaac aggaatatatt tgcagaatat aggtttaact gaatgaagcc atattaataa 1080
45 ctgcattttc ctaactttga aaaattttgc aaatgtctta ggtgatttaa ataaatgagt 1140
46 attgggccta aatgcaacac cagtctgttt tgaacagggt ctattacca gaactttttt 1200
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53 <213> ORGANISM: Homo sapiens
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58 cccgcgggcc agaaggagt cttctaccag cccatgcccc tgaaggctc gctggagatc 180
59 gagtaccaag ttttagatgg agcaggatta gatattgatt tccatcttgc ctctccagaa 240
60 ggcaaaacct tagtttttga acaagaaaa tcagatggag ttcacactgt agagactgaa 300

ENTERED

See p.5

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61 gttggtgatt acatgttctg ctttgacaat acattcagca ccatttctga gaaggtgatt 360
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63 aaatatatta ctggcacaga tatattggat atgaaactgg aagacatcct ggaatccatc 480
64 aacagcatca agtccagact aagcaaaagt gggcacatac aaactctgct tagagcattt 540
65 gaagctcgtg atcgaaacat acaagaaaagc aactttgata gagtcaattt ctggtctatg 600
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72 <212> TYPE: PRT

73 <213> ORGANISM: Homo sapiens

75 <400> SEQUENCE: 3

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82 Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
83           35           40           45
85 Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
86           50           55           60
88 Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu
89   65           70           75           80
91 Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
92           85           90           95
94 Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
95           100          105          110
97 Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn
98           115          120          125
100 Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr
101           130          135          140
103 Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile
104 145          150          155          160
106 Asn Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Thr Leu
107           165          170          175
109 Leu Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe
110           180          185          190
112 Asp Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val
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123 <211> LENGTH: 15

124 <212> TYPE: PRT

125 <213> ORGANISM: Artificial Sequence

127 <220> FEATURE:

128 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic

130 <400> SEQUENCE: 4

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138 <213> ORGANISM: Artificial Sequence
140 <220> FEATURE:
141 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
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150 <212> TYPE: DNA
151 <213> ORGANISM: Homo sapiens
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156 ggatacagtc actctggaag tattagtggc tccagcagtt ccatcatgtg aagtaccctc 180
157 ttctgctctg agtggaaactg tggatatct acgatgtcaa gacaaagaag ggaatccagc 240
158 tcctgaatac acatggttta aggatggcat ccgtttgcta gaaaatccca gacttggctc 300
159 ccaaagcacc aacagctcat acacaatgaa tacaaaaact ggaactctgc aatttaatac 360
160 tgtttccaaa ctggacactg gagaatattc ctgtgaagcc cgcaattctg ttggatatcg 420
161 caggtgtcct gggaaacgaa tgcaagtaga tgatctcaac ataagtggca tcatagcagc 480
162 cgtagtagtt gtggccttag tgatttcctt ttgtggcctt ggtgtatgct atgctcagag 540
163 gaaaggctac ttttcaaaaag aaacctcctt ccagaagagt aattcttcat ctaaagccac 600
164 gacaatgagt gaaaatgatt tcaagcacac aaaatccttt ataatttaaa gactccactt 660
165 tagagataca ccaaagccac cgttgttaca caagttatta aactattata aaactctgct 720
166 ttgtccgaca ttgcaaaga ggtacacgag gaaatggaat tggattttca ttttaatttt 780
167 catgactact aactcacctg aacttgctat tttaaacaaa tagttctgtc gacacctaaa 840
168 atataatctg gcttcttgtg tctggactaa gttaaaagaa ttaaaatact ttgtaatgtc 900
169 aaaaaa
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173 <211> LENGTH: 215
174 <212> TYPE: PRT
175 <213> ORGANISM: Homo sapiens
177 <400> SEQUENCE: 7
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181 Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser Ala Pro Ser
182           20           25           30
184 Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu Glu Val Leu
185           35           40           45
187 Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser Ala Leu Ser
188           50           55           60
190 Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly Asn Pro Ala
191   65           70           75           80
193 Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu Glu Asn Pro
194           85           90           95

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196 Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met Asn Thr Lys
197      100      105      110
199 Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp Thr Gly Glu
200      115      120      125
202 Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg Cys Pro Gly
203      130      135      140
205 Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile Ile Ala Ala
206 145      150      155      160
208 Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu Gly Val Cys
209      165      170      175
211 Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser Phe Gln Lys
212      180      185      190
214 Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn Asp Phe Lys
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217 His Thr Lys Ser Phe Ile Ile
218      210      215
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222 <211> LENGTH: 15
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243 <212> TYPE: DNA
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249 aaagctacac aaaaagcctg gatcactcat cgaaccaccc ctgaagccag tgaaggctct 180
250 ctgcctcgcc cctctagcgt tcgtctggag tagcgccacc ccggttctct ggggacacag 240
251 gggttgccacc atggggccca ccagcgtccc gctgggtcaag gccaccgca gctcgggtctc 300
252 tgactacgtc aactatgata tcatcgctccg gcattacaac tacacgggaa agctgaatat 360
253 cagcgcgagc aaggagaaca gcattaaact gacctcggtg gtgttcattc tcatctgctg 420
254 ctttatcatc ctggagaaca tctttgtctt gctgaccatt tggaaaacca agaaattcca 480
255 ccgacccatg tactatttta ttggcaatct ggccctctca gacctgttgg caggagtagc 540
256 ctacacagct aacctgctct tgtctggggc caccacctac aagctcactc ccgccagtgt 600
257 gtttctgcgg gaagggagta tgtttgtggc cctgtcagcc tccgtgttca gtctcctcgc 660
258 catcgccatt gagcgctata tcacaatgct gaaaatgaaa ctccacaacg ggagcaataa 720
259 cttccgcctc ttctgtctaa tcagcgctgt ctgggtcatc tccctcatcc tgggtggcct 780
260 gcctatcatg ggctggaact gcatacgtgc gctgtccagc tgctccaccg tgctgccgct 840

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263	ccgcaagaac	atttccaagg	ccagccgcag	ctctgagaat	gtggcgctgc	tcaagaccgt	1020
264	aattatcgtc	ctgagcgtct	tcatcgctg	ctgggcaccg	ctcttcaccc	tgctcctgct	1080
265	ggatgtgggc	tgcaaggtga	agacctgtga	catcctcttc	agagcggagt	acttctgtgt	1140
266	gttagctgtg	ctcaactccg	gcaccaaccc	catcatttac	actctgacca	acaaggagat	1200
267	gcgtcgggcc	ttcattccgga	tcatgtcctg	ctgcaagtgc	ccgagcggag	actctgctgg	1260
268	caaattcaag	cgacccatca	tcgccggcat	ggaattcagc	cgcagcaaat	cggacaattc	1320
269	ctcccacccc	cagaaagacg	aaggggacaa	cccagagacc	attatgtctt	ctggaaacgt	1380
270	caactcttct	tcctagaact	ggaagctgtc	caccacaccg	aagcgctctt	tacttggtcg	1440
271	ctggccaccc	cagtgttttg	aaaaaaatct	ctgggcttcg	actgctgcca	gggaggagct	1500
272	gctgcaagcc	agagggagga	agggggagaa	tacgaacagc	ctggtggtgt	cgggtgttgg	1560
273	tgggtagagt	tagttcctgt	gaacaatgca	ctgggaaggg	tgagatcag	gtcccggcct	1620
274	ggaatatata	ttctaccccc	ctggagcttt	gattttgcac	tgagccaaa	gtctagcatt	1680
275	gtcaagctcc	taaagggttc	atttggcccc	tcttcaaga	ctaattgtccc	catgtgaaag	1740
276	cgctctcttg	tctggagctt	tgaggagatg	tttctcttca	ctttagtttc	aaacccaagt	1800
277	gagtgtgtgc	acttctgctt	ctttagggat	gccctgtaca	tcccacaccc	cacctccct	1860
278	tcccttcata	ccccctctca	acgttctttt	actttatact	ttaactacct	gagagtattc	1920
279	agagctgggg	ttgtggaatg	atcgatcatc	tatagcaa	aggctatgtt	gagtacgtag	1980
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282	aaaacatctt	ttcaatgaaa	tgtgttacca	tttcataatc	attgaagccg	aaatctgcat	2160
283	aaggaagccc	actttatcta	aatgatatta	gccaggatcc	ttggtgtcct	aggagaaaca	2220
284	gacaagcaaa	acaaagtga	aaccgaatgg	attaactttt	gcaaaccaag	ggagatttct	2280
285	tagcaaatga	gtctaacaaa	tatgacatcc	gtctttccca	cttttgttga	tgtttatttc	2340
286	agaatcttgt	gtgattcatt	tcaagcaaca	acatgttgta	ttttgttgtg	ttaaaggtac	2400
287	ttttcttgat	ttttgaatgt	atttgtttca	ggaagaagtc	attttatgga	tttttctaac	2460
288	ccgtgttaac	ttttctagaa	tccacctctt	tgtgccctta	agcattactt	taactggtag	2520
289	ggaacgccag	aacttttaag	tccagctatt	cattagatag	taattgaaga	tatgtataaa	2580
290	tattacaaag	aataaaaaata	tattactgtc	tctttagtat	ggttttcagt	gcaattaaac	2640
291	cgagagatgt	cttgtttttt	taaaaagaat	agtattttaat	aggtttctga	cttttgtgga	2700
292	tcatttttgca	catagcttta	tcaactttta	aacattaata	aactgatttt	tttaaaq	2757

295 <210> SEQ ID NO: 11

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296 <211> LENGTH: 1146
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297 <212> TYPE: DNA

298 <213> ORGANISM: Homo sapiens

300 <400> SEQUENCE: 11

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302	aactatgata	tcatcgtcg	gcattacaac	tacacgggaa	agctgaatat	cagcgcggac	120
303	aaggagaaca	gcattaaact	gacctcgggtg	gtgttcattc	tcatctgctg	ctttatcatc	180
304	ctggagaaca	tctttgtctt	gctgaccatt	tggaaaacca	agaaattcca	ccgacccatg	240
305	tactatttta	ttggcaatct	ggccctctca	gacctgttg	caggagtagc	ctacacagct	300
306	aacctgctct	tgtctggggc	caccacctac	aagctcactc	ccgccagtg	gtttctgcgg	360
307	gaagggagta	tgtttggtgc	cctgtcagcc	tccgtgttca	gtctcctcgc	catcgccatt	420
308	gagcgctata	tcacaatgct	gaaaatgaaa	ctccacaacg	ggagcaataa	cttcgcctc	480
309	ttcctgctaa	tcagcgctgc	ctgggtcatc	tccctcatcc	tgggtggcct	gcctatcatg	540
310	ggctggaact	gcatacgtgc	gctgtccagc	tgtccaccg	tgctgcgcct	ctaccacaag	600
311	cactatatcc	tcttctgcac	cacggtcttc	actctgcttc	tgctctccat	cgtcattctg	660
312	tactgcagaa	tctactcctt	ggtcaggact	cggagccgcc	gcctgacgtt	ccgcaagaac	720

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

file:///C:/CITS/OUTBOUND/vs1105/57/7/7.htm

6/6/01

VERIFICATION SUMMARY

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L:775 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19

L:821 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20

L:890 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22